


```
*          *          *          *          *          *          *          *
CTG CAA ATG AAC AGC CTG AGA GGT' GAG GAC ACG GC'T GTG TAT TAC TGTT
L   Q   M   N   S   L   R   A   E   D   T   A   V   Y   Y   C>
_a _a _a TRANSLATION OF 7A3 VH.SEQ [A]_a _a _a _a _a _a >

290      300      310      320      330
*        *        *        *        *
GGG AAA ACT GGG GAA TAT AGT GGC TAC GAT TCT AGT GGT GTG GAC GTC
A K T G E Y S G G Y D S S G V D V>
_a _a _a TRANSLATION OF 7A3 VH.SEQ [A]__a __a __a __a __a __a >

340           350           360
*             *             *
TGG GGC AAA GGG ACC ACG GTC ACC GTC TCC TCA (SEQ ID NO:7)
W G K G T T V T V S S> (SEQ ID NO:8)
_a TRANSLATION OF 7A3 VII.SEQ [A]____a ____>
```

(ii) 1A-E5 VII

Sequence Range: 1 to 345

	10	20	30	40
* GAG GTG CAG CTG GTG GAG TCT GGT GGA GGC TTA GTT CAG CCT GGG GGG				
E. V Q L V E S G G L V Q P G G>				
a a a a TRANSLATION OF 1AE-5 VH [A] a a a a				
50 *	60 *	70 *	80 *	90 *
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAC				
S L R L S C A A S G F T F S S Y>				
a a a a TRANSLATION OF 1AE-5 VH [A] a a a a				
100 *	110 *	120 *	130 *	140 *

TGG ATG CAC TGG GTC CGC CAA GCT CCA GGG AAG GGG CTG GTG TGG GTC
W M H W V R Q A P G K G L V W V>
_a_a_a_a_translation of 1AE-5 VH [A]_a_a_a_a_>

150 * * 160 * * 170 * * 180 * * 190 *
* * * * * * * * * *
TCA CGT ATT AAT AGT GAT GGG AGT AGC ACA AGC TAC GCG GAC TCC GTG
S R I N S D G S S 'T' S Y A D S V>
_a_a_a_a_translation of 1AE-5 VH [A]_a_a_a_a_>

200 * * 210 * * 220 * * 230 * * 240 *
* * * * * * * * * *
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAC GCC AAG AAC ACG CTG TAT
K G R F T I S R D N A K N T L Y>
_a_a_a_a_translation of 1AE-5 VH [A]_a_a_a_a_>

250 * * 260 * * 270 * * 280 *
* * * * * * * * * *
CTG CAA ATG AAC AGT CTG AGA GCC GAG GAC ACG GCC GTG TAT TAC TGT
L Q M N S L R A E D T A V Y Y C>
_a_a_a_a_translation of 1AE-5 VH [A]_a_a_a_a_>

290 * * 300 * * 310 * * 320 * * 330 *
* * * * * * * * * *
GCA AGG GAG AAT AGT TAT GTG CCT TCG GGG CAG GCC ACC CTG GTC ACC
A R E N S Y V P W G Q G T L V T>
_a_a_a_a_translation of 1AE-5 VH [A]_a_a_a_a_>

340

* *
GTC TCC TCA (SEQ ID NO:113)
V S S> (SEQ ID NO:111)
_a_a_a_a_>

Sequence Range: 1 to 354

```

      10      20      30      40
      *      *      *      *
CAG GTG CAA CTG CAG GAG TCG GGG GGA GGC GTG GTC CAG CCT GGG GGG
Q V Q L Q E S G G G V V Q P G G>
_a_a_a_a_a_TRANSLATION OF 1AH-6 VH [A]_a_a_a_a_a_>

      50      60      70      80      90
      *      *      *      *      *
TCC CTG AGA CTC TCC TGT GCA GCG TCT GCA TTC ACC TTC AGT GGC TAT
S L R L S C A A S G F T F S G Y>
_a_a_a_a_a_TRANSLATION OF 1AH-6 VH [A]_a_a_a_a_a_>

      100     110     120     130     140
      *      *      *      *      *
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
G M H W V R Q A P G K G L E W V>
_a_a_a_a_a_TRANSLATION OF 1AH-6 VH [A]_a_a_a_a_a_>

      150     160     170     180     190
      *      *      *      *      *
GCA TCT GTA CGG AAC GAT GGA AGT AAT ACA TAC TAC ACA GAC TCC GTG
A S V R N D G S N T Y Y T D S V>
_a_a_a_a_a_TRANSLATION OF 1AH-6 VH [A]_a_a_a_a_a_>

      200     210     220     230     240
      *      *      *      *      *
AAG GGC CGA TTC ACC ATC CCC AGA GAC AAC ACC AAG AAC ACG CTG TAT
K G R F T I P R D N T K N T L Y>
_a_a_a_a_a_TRANSLATION OF 1AH-6 VH [A]_a_a_a_a_a_>

      250     260     270     280
      *      *      *      *
CTG CAA ATG AAC AGC CTG AGA GCC GAG GAC ACG GCC GTA TAT TAC TGT
L Q M N S L R A E D T A V Y Y C>

```


FIG. 1(b) (i) $\frac{7A3}{VI.}$

			10			20			30			40	
	*	*	*	*	*	*	*	*	*	*	*	*	*
GAC	ATC	GTG	ATG	ACC	CAG	TCT	CCA	GAC	TCC	CTG	GCT	GTG	TCT
D	I	V	M	T	Q	S	P	D	S	L	A	V	S
a a a TRANSLATION OF 7A3 VL.SEQ [A] a a a a a													
50			60			70			80			90	
*	*	*	*	*	*	*	*	*	*	*	*	*	*
GAG	AGG	GCC	ACC	ATC	AAC	TGC	AAG	TCC	AGC	CAG	AGT	CTT	TTA
E	R	A	T	I	N	C	K	S	S	Q	S	L	L
a a a TRANSLATION OF 7A3 VL.SEQ [A] a a a a a													
100			110			120			130			140	
*	*	*	*	*	*	*	*	*	*	*	*	*	*
TAC	AAC	AAG	ATG	AAC	TAC	TTA	GCT	TGG	TAC	CAG	CAG	AAA	CCA
Y	N	K	M	N	Y	L	A	W	Y	Q	Q	K	P
a a a TRANSLATION OF 7A3 VL.SEQ [A] a a a a a													
150			160			170			180			190	
*	*	*	*	*	*	*	*	*	*	*	*	*	*
CCT	CCT	AAG	CTG	CTC	ATT	AAC	TGG	GCA	TCT	ACC	CGG	GAA	TCC
P	P	K	L	L	I	N	W	A	S	T	R	E	S
a a a TRANSLATION OF 7A3 VL.SEQ [A] a a a a a													
200			210			220			230			240	
*	*	*	*	*	*	*	*	*	*	*	*	*	*
CCT	GAC	CGA	TTC	AGT	GGC	AGC	GGG	TCT	GGG	ACA	GAT	TTC	ACT
P	D	R	F	S	G	S	G	S	G	T	D	F	T
a a a TRANSLATION OF 7A3 VL.SEQ [A] a a a a a													

_____a____a____a____TRANSLATION OF 7A3 VL.SEQ [A]____a____a____a____>
250 260 270 280
* * * * *
ATC AGC AGC CTG CAG GCT GAA GAT GTG GCA GTT TAT TAC TGT CAG CAA
I S S L Q A E D V A V Y C Q Q>
_____a____a____a____TRANSLATION OF 7A3 VL.SEQ [A]____a____a____a____>
290 300 310 320 330
* * * * *
TAT TAT GCA ACT CCT CTG ACG TTC GGC CAC GGG ACC AAG GTG GAA ATC
Y Y A T P L T F G H G T K V E I>
_____a____a____a____TRANSLATION OF 7A3 VL.SEQ [A]____a____a____a____>
340
*
AAA CGT (SEQ ID NO:15)
K R> (SEQ ID NO:16)
_____a____>

FIG. 1(b)(ii) 10A6 VL

Sequence Range: 1 to 357

10 20 30 40
* * * * *
CAC GTT ATA CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG
H V I L T Q D P A V S V A L G Q>
_____a____a____a____TRANSLATION OF 10A6 VL.SEQ [A]____a____a____a____>
50 60 70 80 90
* * * * *
ACA GTC AGG ATC ACG TGC CAA GGA GAC AGC CTC AAA AGC TAC TAT GCA
T V R I T C Q G D S L K S Y Y A>
_____a____a____a____TRANSLATION OF 10A6 VL.SEQ [A]____a____a____a____>
100 110 120 130 140

Figure 1 (c) Antibodies to TGFbeta1 isolated from CDR3 spiking experiment

FIG. 1(c) (i) 27C1_VH

Sequence Range: 1 to 369

GCG CGA ACT GGT GAA TAT AGT GGC TAC GAC ACG AGT GGT GTG GAG CTC
 A R T G E Y S G Y D T S G V E L>
 _a_a_a_a_TRANSLATION OF 27C1 VII.SEQ [A]_a_a_a_a_a_>

340 * 350 360
 * * * * *
 TGG GGG CAA GGG ACC ACG GTC ACC GTC TCC TCA (SEQ ID NO:11)
 W G Q G T T V T V S S> (SEQ ID NO:12)
 _a_a_TRANSLATION OF 27C1 VII.SEQ [A]_a_a_a_>

Figure 2. Sequences of antibodies specific for TGFbeta2

(a) Antibodies to TGFbeta 2 isolated directly from repertoires

FIG 2.(a) (i) 2A-H11 VH (also known as 6H1 VH)

Sequence Range: 1 to 345

[illegible]

250	260	270	280
* * *	* * *	* * *	* * *
CTG CAA ATG GAC AGC CTG AGA GCC GAG GAC ACC GCC GTG TAT TAC TGT			
L Q M D S L R A E D T A V Y Y C>			
_a_a_a_ TRANSLATION OF 6H1 VH.SEQ [A]_a_a_a_a_>			
290	300	310	320
* * *	* * *	* * *	* * *
GGA AGA ACG CTG GAG TCT AGT TTG TGG GGC CAA GGC ACC CTG GTC ACC			
G R T L E S S L W G Q G T L V T>			
_a_a_a_ TRANSLATION OF 6H1 VH.SEQ [A]_a_a_a_a_>			
340			
* *			
GTC TCC TCA (SEQ ID NO:5)			
V S S> (SEQ ID NO:6)			
_a_a_a_>			

FIG 2.(a)(ii) 2A-λ9 (also known as 11E6 VII)

Sequence Range: 1 to 350

[illegible]

GCT ATG CAC TGG GTC CGC CAG GCT CCA GCC AAG GGG CTG GAG TGG GTG
 A M H W V R Q A P A K G L E W V>
 _a_a_a_ TRANSLATION OF 11E6 VH.SEQ [A]_a_a_a_a_>

150 * * 160 * * 170 * * 180 * * 190 *
 * * * * * * * * * *
 GCA GTT ATA TCA TAT GAT GGA AGC AAT AAA TAC TAC GCA GAC TCC GTG
 A V I S Y D G S N K Y Y A D S V>
 _a_a_a_ TRANSLATION OF 11E6 VH.SEQ [A]_a_a_a_a_>

200 * * 210 * * 220 * * 230 * * 240 *
 * * * * * * * * * *
 AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT
 K G R F T I S R D N S K N T L Y>
 _a_a_a_ TRANSLATION OF 11E6 VH.SEQ [A]_a_a_a_a_>

250 * * 260 * * 270 * * 280 * *
 * * * * * * * * * *
 CTG CAA ATG AAC AGC CTG AGA GCT GAG GAC ACG GCC GTG TAT TAC TGT
 L Q M N S L R A E D T A V Y Y C>
 _a_a_a_ TRANSLATION OF 11E6 VH.SEQ [A]_a_a_a_a_>

290 * * 300 * * 310 * * 320 * * 330 *
 * * * * * * * * * *
 GCA AGA GCG GGG TTG GAA ACG ACG TGG GGC CAA GGA ACC CTG GTC ACC
 A R A G L E T T W G Q G T L V T>
 _a_a_a_ TRANSLATION OF 11E6 VH.SEQ [A]_a_a_a_a_>

340 * * 350 *
 * * * * *
 GTC TCC TCA AGT GG (SEQ ID NO:36)
 V S S S G> (SEQ ID NO:37)
 _TRANSLATION_a_>

FIG 2.(a)(iii) Gold11-VH

Sequence Range: 1 to 369

```

      10      20      30      40
      *      *      *      *
CAG GTC ACC TTG AAG GAG TCT GGG GGA AGC GTG GTC CAG CCT GGG AGG
Q  V  T  L  K  E  S  G  G  S  V  V  Q  P  G  R>
_a_a_a_a_a_TRANSLATION OF GOLD11-VH [A]_a_a_a_a_a_>

      50      60      70      80      90
      *      *      *      *      *
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT
S  L  R  L  S  C  A  A  S  G  F  T  F  S  S  Y>
_a_a_a_a_a_TRANSLATION OF GOLD11-VH [A]_a_a_a_a_a_>

     100     110     120     130     140
      *      *      *      *      *
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGG CTG GAG TGG GTG
G  M  H  W  V  R  Q  A  P  G  K  G  L  E  W  V>
_a_a_a_a_a_TRANSLATION OF GOLD11-VH [A]_a_a_a_a_a_>

     150     160     170     180     190
      *      *      *      *      *
GCA GTT ATA TCA TAT GAT GGA AGT AAT AAA TAC TAT GCA GAC TCC GTG
A  V  I  S  Y  D  G  S  N  K  Y  Y  A  D  S  V>
_a_a_a_a_a_TRANSLATION OF GOLD11-VH [A]_a_a_a_a_a_>

     200     210     220     230     240
      *      *      *      *      *
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CAG TAT
K  G  R  F  T  I  S  R  D  N  S  K  N  T  Q  Y>
_a_a_a_a_a_TRANSLATION OF GOLD11-VH [A]_a_a_a_a_a_>

     250     260     270     280

```



```

*      *      *      *      *      *      *      *
CTG CAA ATG AAC AGC CTG AGA GCT GAA GAC ACG GCA GAG TAT TAC TGT
L   Q   M   N   S   L   R   A   E   D   T   A   E   Y   Y   C>
_a_a_a_a_a_translation OF GOLD11-VH [A]_a_a_a_a_a_>

290      300      310      320      330
*      *      *      *      *
GGG AGA ACT GGG GAA TAT AGT GGC CAC GCA TCT ACT GGA GAG AAC GTC
A   R   T   G   E   Y   S   G   H   A   S   T   G   E   N   V>
_a_a_a_a_a_translation OF GOLD11-VH [A]_a_a_a_a_a_>

340      350      360
*      *      *
TGG GGC CGG GGC ACC CTG GTC ACC GTC TCG AGT (SEQ ID NO:115)
W   G   R   G   T   L   V   T   V   S   S> (SEQ ID NO:116)
_a_a_a_a_a_translation OF GOLD11-VH [A]_a_a_a_a_a_>

10      20      30      40
*      *      *      *
TCC TAT GTG CTG ACT CAC CCC CCC TCA GTG TCT GGG ACC CCC GGG CAG
S   Y   V   L   T   H   P   P   S   V   S   G   T   P   G   Q>
_a_a_a_a_a_translation OF GOLD11-VL [A]_a_a_a_a_a_>

50      60      70      80      90
*      *      *      *      *
AGA GTC ACC ATC TCT TGT TCT GGA GGC AGA TCC AAC ATC GGC AGT AAT
R   V   T   I   S   C   S   G   G   R   S   N   I   G   S   N>
_a_a_a_a_a_translation OF GOLD11-VL [A]_a_a_a_a_a_>

100      110      120      130      140
*      *      *      *      *
ACT GTA AAG TGG TAT CAG CAG CTC CCA GGA ACG CCC CCC AAA CTC CTC
T   V   K   W   Y   Q   Q   L   P   G   T   P   P   K   L   L>

```

FIG 2.(a)(iv) GOLD11-VL

Sequence Range: 1 to 336

```

_a_a_a_a_translation OF GOLD11-VL [A]_a_a_a_a_a_>
150 * * * * * 160 * * * * * 170 * * * * * 180 * * * * * 190 *
ATC TAT GGC AAT GAT CAG CGG CCC TCA GGG ATC CCT GAC CGA TTC TCT
I Y G N D Q R P S G I P D R F S>
_a_a_a_a_a_translation OF GOLD11-VL [A]_a_a_a_a_a_>
200 * * * * * 210 * * * * * 220 * * * * * 230 * * * * * 240 *
GGC TCC AAG TCT GGC ACC TCA GCC TCC CTG GCC ATC ACT GGG GTC CAG
G S K S G T S A S L A I T G V Q>
_a_a_a_a_a_translation OF GOLD11-VL [A]_a_a_a_a_a_>
250 * * * * * 260 * * * * * 270 * * * * * 280 * * * * *
GCT GAA GAC GAG GCT GAT TAT TAC TGC CAG TCA TAT GAC AGC AGC CTG
A E D E A D Y Y C Q S Y D S S L>
_a_a_a_a_a_translation OF GOLD11-VL [A]_a_a_a_a_a_>
290 * * * * * 300 * * * * * 310 * * * * * 320 * * * * * 330 *
AGG GGT TCG AGG GTC TTC GGA ACT GGG ACC AAG GTC ACC GTC CTA GGT (SEQ ID NO:117)
R G S R V F G T G T K V T V L G> (SEQ ID NO:118)
_a_a_a_a_a_translation OF GOLD11-VL [A]_a_a_a_a_a_>
340 * * * * * 350 * * * * * 360 * * * * * 370 * * * * * 380 *
CAG GTA CAA CCT CAG CAG TCT GGG GGA GAG GTG AAG CAG CCT GGG GCC
Q V Q P Q Q S G G E V K Q P G A>
_a_a_a_a_a_translation OF 1-G2-VII [A]_a_a_a_a_a_>
50 * * * * * 60 * * * * * 70 * * * * * 80 * * * * * 90 *

```

FIG 2.(a)(v)
1-G2

Sequence Range: 1 to 381

```

*      *      *      *      *      *      *      *
TCC GTG AAG GTT TCC TGT AAG GCG TCT GGA TAC ACC TTC ACC AGC TTC
S   V   K   V   S   C   K   A   S   G   Y   T   F   T   S   F>
_a_a_a_a_a_translation of 1-G2-VH [A]_a_a_a_a_a_>

100      110      120      130      140
*      *      *      *      *
TAT ATG AAC TGG GTG CGA CAG GCC CCC GGA CAA GGG CTT GAG TGG ATG
Y   M   N   W   V   R   Q   A   P   G   Q   G   L   E   W   M>
_a_a_a_a_a_translation of 1-G2-VH [A]_a_a_a_a_a_>

150      160      170      180      190
*      *      *      *      *
GGA ATA ATC AGC CCT CGT GGT GGT ACC ACA AGT TAC GCA CAG AAC TTC
G   I   I   S   P   R   G   G   T   T   S   Y   A   Q   N   F>
_a_a_a_a_a_translation of 1-G2-VH [A]_a_a_a_a_a_>

200      210      220      230      240
*      *      *      *      *
CAG GGC AGA GTC ACC ATG ACC AGG GAC AGC TCC ACA AGC ACA GTC TAC
Q   G   R   V   T   M   T   R   D   T   S   T   S   T   V   Y>
_a_a_a_a_a_translation of 1-G2-VH [A]_a_a_a_a_a_>

250      260      270      280
*      *      *      *
ATG GAG CTG AGC AGC CTG AGA TCT GAG GAC AGC GCC GTG TAT TAT TGT
M   E   L   S   S   L   R   S   E   D   T   A   V   Y   Y   C>
_a_a_a_a_a_translation of 1-G2-VH [A]_a_a_a_a_a_>

290      300      310      320      330
*      *      *      *      *
GCG ATA ATT GGG GGT ACT ACT ATG AGA GTA GGG GGG CCC GAT GCT TTT
A   I   I   G   G   T   T   M   R   V   G   G   P   D   A   F>
_a_a_a_a_a_translation of 1-G2-VH [A]_a_a_a_a_a_>

340      350      360      370      380
*      *      *      *      *

```

FIG 2.(a)(vi)
1-H6

Sequence Range: 1 to 381

	10	20	30	40	
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	
GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG					
E V Q L V E S G G G V V Q P G R>					
a a a a a TRANSLATION OF 1-H6 VH [A]	a	a	a	a	a
50	60	70	80	90	
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	
TCC CTG AGA CTC TCC TGT GCA GCG TCT' GGA TTC ACC TTC AGG AAC TAT					
S L R L S C A A S G F T F R N Y>					
a a a a a TRANSLATION OF 1-H6 VH [A]	a	a	a	a	a
100	110	120	130	140	
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC AAG GGC CTG GAG TGG GTG					
G M H W V R Q A P G K G L E W V>					
a a a a a TRANSLATION OF 1-H6 VH [A]	a	a	a	a	a
150	160	170	180	190	
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	
GCA GTT ATA TGG TAT GAT GGA AGT AAT AAA TAC TAT GCA GAC TCC GTG					
A V I W Y D G S N K Y Y A D S V>					
a a a a a TRANSLATION OF 1-H6 VH [A]	a	a	a	a	a
200	210	220	230	240	
* * * * *	* * * * *	* * * * *	* * * * *	* * * * *	
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT					

K G R F T I S R D N S K N T L Y>
 _a_a_a_a_ TRANSLATION OF 1-H6 VII [A] _a_a_a_a_a_>

250 * * * * * 270 * * * * * 280 * * * * *
 CTG CAA ATG AAC AGC CTG AGA GTC GAG GAC ACG GCT GTT TAT TAC TGT
 L Q M N S L R V E D T A V Y Y C>
 _a_a_a_a_a_ TRANSLATION OF 1-H6 VII [A] _a_a_a_a_a_>

290 * * * * * 310 * * * * * 320 * * * * * 330 * * * * *
 GCG AGA AGA TGG TAT GGT GGC AGT GGT TAT TGG GGC CAC TTC TAC TCC
 A R R W Y G G S G Y W G H F Y S>
 _a_a_a_a_a_ TRANSLATION OF 1-H6 VII [A] _a_a_a_a_a_>

340 * * * * * 350 * * * * * 360 * * * * * 370 * * * * * 380 * * * * *
 TAC ATG GAC GGC TGG GGC AAA GGC ACC AAG GTC ACC GTC TCC TCA (SEQ ID NO:121)
 Y M D G W G K G T K V T V S S> (SEQ ID NO:122)
 _a_a_a_a_a_ TRANSLATION OF 1-H6 VII [A] _a_a_a_a_a_>

Figure 2(b) (i)

```

10      20      30      40
GAT GTT GTG ATG ACT CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA
D V V M T Q S P S S L S A S V G>

50      60      70      80      90
GAC AGA GTC ACC ATC ACT TGC CGG GCC AGT CAG GGC ATT AGC AAT TAT
D R V T I T C R A S Q G I S N Y>

100     110     120     130     140
TTA GCC TGG TAT CAG CAA AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC
L A W Y Q Q K P G K A P K L L I>

150     160     170     180     190
TAT AAG GCA TCT ACT TTA GAA AGT GGG GTC CCA TCA AGG TTC AGT GGC
Y K A S T L E S G V P S R F S G>

200     210     220     230     240
AGT GGA TCT GGG ACA GAA TTC ACT CTC ACA ATC AGC AGT CTG CAA CCT
S G S G T E F T L T I S S L Q P>

250     260     270     280
GAA GAT TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CCT CGA
E D F A T Y Y C Q Q S Y S T P R>

290     300     310     320     330
ACG TTC GGC CAA GGG ACC AAA GTG GAT ATC AAA CGT (SEQ ID NO:38)
T F G Q G T K V D I K R (SEQ ID NO:39)

```

Figure 2(b) (ii)

```

10  TCG TCT GAG CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG
   S  S  E  L  T  Q  D  P  A  V  S  V  A  L  G  Q>
20
30
40
50  ACA GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA
   T  V  R  I  T  C  Q  G  D  S  L  R  S  Y  Y  A>
60
70
80
90
100 AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC ATC TAT
   S  W  Y  Q  Q  K  P  G  Q  A  P  V  L  V  I  Y>
110
120
130
140
150 GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC GAC TTC GCT GGC TCC
   G  K  N  N  R  P  S  G  I  P  D  R  F  A  G  S>
160
170
180
190
200 AAC TCA GGA AAC ACA GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAG
   N  S  G  N  T  A  S  L  T  I  T  G  A  Q  A  E>
210
220
230
240
250 GAT GAG GCT GAC TAT TAC TGT AGC TCC CGG GAC AGC AGT GGT AAC CAT
   D  E  A  D  Y  Y  C  S  S  R  D  S  S  G  N  H>
260
270
280
290 GTG GTT TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT (SEQ ID NO:40)
   V  V  F  G  G  G  T  K  L  T  V  L  G> (SEQ ID NO:41)
300
310
320

```

Figure 2(b) (iii)

```

10      TCG TCT GAG CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG
      S  S  E  L  T  Q  D  P  A  V  S  V  A  L  G  Q>
20
30
40
50      ACA GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA
      T  V  R  I  T  C  Q  G  D  S  L  R  S  Y  Y  A>
60
70
80
90
100     AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC ATC TAT
      S  W  Y  Q  Q  K  P  G  Q  A  P  V  L  V  I  Y>
110
120
130
140
150     GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC CGA TTC TCT GGC TCC
      G  K  N  N  R  P  S  G  I  P  D  R  F  S  G  S>
160
170
180
190
200     AGC TCA GGA AAC ACA GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAA
      S  S  G  N  T  A  S  L  T  I  T  G  A  Q  A  E>
210
220
230
240
250     GAT GAG GCT GAC TAT TAC TGT AAC TCC CGG GAC AGC AGT AGT ACC CAT
      D  E  A  D  Y  Y  C  N  S  R  D  S  S  S  T  H>
260
270
280
290     CGA GGG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT (SEQ ID NO:42)
      R  G  V  F  G  G  G  T  K  L  T  V  L  G  (SEQ ID NO:43)
300
310
320
330

```


Figure 2(b) (iv)

```

10  GAA GTT GTG CTG ACT CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA
    E  V  V  L  T  Q  S  P  S  S  L  S  A  S  V  G>
20
30
40
50  GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT GGA GAT GAT
    D  R  V  T  I  T  C  R  A  S  Q  G  I  G  D  D>
60
70
80
90
100 TTG GGC TGG TAT CAG CAG AAG CCA GGG AAA GCC CCT ATC CTC CTG ATC
    L  G  W  Y  Q  Q  K  P  G  K  A  P  I  L  L  I>
110
120
130
140
150 TAT GGT ACA TCC ACT TTA CAA AGT GGG GTC CCG TCA AGG TTC AGC GGC
    Y  G  T  S  T  L  Q  S  G  V  P  S  R  F  S  G>
160
170
180
190
200 AGT GGA TCT GGC ACA GAT TTC ACT CTC ACC ATC AAC AGC CTG CAG CCT
    S  G  S  G  T  D  F  T  L  T  I  N  S  L  Q  P>
210
220
230
240
250 GAA GAT TTT GCA ACT TAT TAC TGT CTA CAA GAT TCC AAT TAC CCG CTC
    E  D  F  A  T  Y  Y  C  L  Q  D  S  N  Y  P  L>
260
270
280
290 ACT TTC GGC GGA GGG ACA CGA CTG GAG ATT AAA CGT (SEQ ID NO:44)
    T  F  G  G  G  T  R  L  E  I  K  R  (SEQ ID NO:45)
300
310
320

```

Figure 2(b) (v)

```

10      TCG TCT GAG CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG
      S  S  E  L  T  Q  D  P  A  V  S  V  A  L  G  Q>
20
30
40
50      ACA GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AAC TAT TAT GCA
      T  V  R  I  T  C  Q  G  D  S  L  R  N  Y  Y  A>
60
70
80
90
100     AAC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC ATC TAT
      N  W  Y  Q  Q  Q  K  P  G  Q  A  P  V  L  V  I  Y>
110
120
130
140
150     GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC CGA TTC TCT GGC TCC
      G  K  N  N  R  P  S  G  I  P  D  R  F  S  G  S>
160
170
180
190
200     AGC TCA GGG AAC ACA GCT TCC TTG ACC ATC ACT GGG GCT CGG GCG GAA
      S  S  G  N  T  A  S  L  T  I  T  G  A  R  A  E>
210
220
230
240
250     GAT GAG GGT GTC TAT TAC TGT AAC TCC CGG GAC AGC AGT GGT GCG GTT
      D  E  G  V  Y  Y  C  N  S  R  D  S  S  G  A  V>
260
270
280
290     TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT (SEQ ID NO:46)
      F  G  G  G  T  K  L  T  V  L  G  G  (SEQ ID NO:47)
300
310
320

```

FIG. 2(b)(vi)

6H1_VL

Sequence Range: 1 to 324

```

      10      20      30      40
* * * * *
GAA GTT GTG CTG ACT CAG TCT CCA TCC TCC CTG TCT GCA TCT GTA GGA
E V V L T Q S P S S L S A S V G>
_a_a_a_translation of 11E6 VL.SEQ [A]_a_a_a_a_a_>

50      60      70      80      90
* * * * *
GAC AGA GTC ACC ATC ACT TGC CGG GCA ACT CAG GGC ATT GGA GAT
D R V T I T C R A S Q G I G D D>
_a_a_a_translation of 11E6 VL.SEQ [A]_a_a_a_a_a_>

100     110     120     130     140
* * * * *
TTG GGC TGG TAT CAG CAG AAG CCA GGG AAA GCC CCT ATC CTC CTG ATC
L G W Y Q Q K P G K A P I L L I>
_a_a_a_translation of 11E6 VL.SEQ [A]_a_a_a_a_a_>

150     160     170     180     190
* * * * *
TAT GGT ACA TCC ACT TTA CAA AGT GGG GTC CCG TCA AGG TTC AGC GGC
Y G T S T L Q S G V P S R F S G>
_a_a_a_translation of 11E6 VL.SEQ [A]_a_a_a_a_a_>

200     210     220     230     240
* * * * *
AGT GGA TCT GGC ACA GAT TTC ACT CTC ACC ATC AAC AGC CTG CAG CCT
S G S G T D F T L T I N S L Q P>
_a_a_a_translation of 11E6 VL.SEQ [A]_a_a_a_a_a_>

250     260     270     280
* * * * *
GAA GAT TTT GCA ACT TAT TAC TGT CTA CAA GAT TCC ATT TAC CCG CTC
E D F A T Y Y C L Q D S N Y P L>
_a_a_a_translation of 11E6 VL.SEQ [A]_a_a_a_a_a_>

290     300     310     320
* * * * *
ACT TTC GGC GGA GGC ACA CGA CTG GAG ATT AAA CGT (SEQ ID NO:123)
T F G G G T R L E I K R> (SEQ ID NO:124)
_a_a_translation of 11E6 VL.SEQ [A]_a_a_a_a_a_>

```

(SEQ ID NOS: 19-35)

PARENT (1-B2)	A R T G E Y S G Y D S S G V D V W
27-C1	A R T G E Y S G Y D T S G V E L W
27-D7	A R T R E Y S G H D S S G V D D W
27-E10	A R T G P F S G Y D S S G E D V R
27-H1	A R T E E Y S G Y D S S G V D V W
27-E2	A Q T R E Y T G Y D S S G V D V W
28-A11	A R T E E Y S G F D S T G E D V W
28-E12	A R T E E F S G Y D S S G V D V W
28-H10	A R T G E Y S G Y H S S G V D V R
31-G2	A R T E E F S G Y D S S G V D V W
30-B6	A R A G P F S G Y D S S G E D V R
30-E9	A R T G P F S G Y D S S G E D V W
30-F6	A R T E E F S G Y D S S G V D V W
30-D2	A R T G E Y S G Y D S S G E L V W
31-A2	A R T E E F S G Y D S T G E E V W
31-E11	A R T E E F S G Y D S S G V D V W
31-F1	A R T G E Y S G Y D S S G E D V W

FIGURE 3

Figure 4

```

10      TCG TCT GAG CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG
      S S E L T Q D P A V S V A L G Q>
20
30
40
50      ACA GTT AGG ATC ACT TCC CAA GGA GAC AGT CTC AGA AGC TAT TAC ACA
      T V R I T S Q G D S L R S Y Y T>
60
70
80
90
100     AAC TGG TTT CAG CAG AAG CCA GGA CAG CCC CCT CTA CTT GTC GTC TAT
      N W F Q Q K P G G Q P L L V Y>
110
120
130
140
150     GCT AAA AAT AAG CGG CCC TCA GGG ATC CCA GAC CGA TTC TCT GGC TCC
      A K N K R P S G I P D R F S G S>
160
170
180
190
200     AGC TCA GGA AAC ACA GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAA
      S S G N T A S L T I T G A Q A E>
210
220
230
240
250     GAT GAG GCT GAC TAT TAC TGT CAT TCC CGG GAC AGC AGT GGT AAC CAT
      D E A D Y Y C H S R D S S G N H>
260
270
280
290     GTG CTT TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT (SEQ ID NO:48)
      V L F G G G T K L T V L G (SEQ ID NO:49)
300
310
320

```

(SEQ ID NOS: 50-52)

```

H
i
n
d
I
I
I (SEQ ID NO:50) ---
aagcttgccgcacccatggactggacctggcgcggtgtttttgcctgctcgccgtggccccc
1 -----+-----+-----+-----+-----+ 60
ttcgaaacggcggtggtacctgacctggaccgcgcacaaaacggacgagcggcacccggga

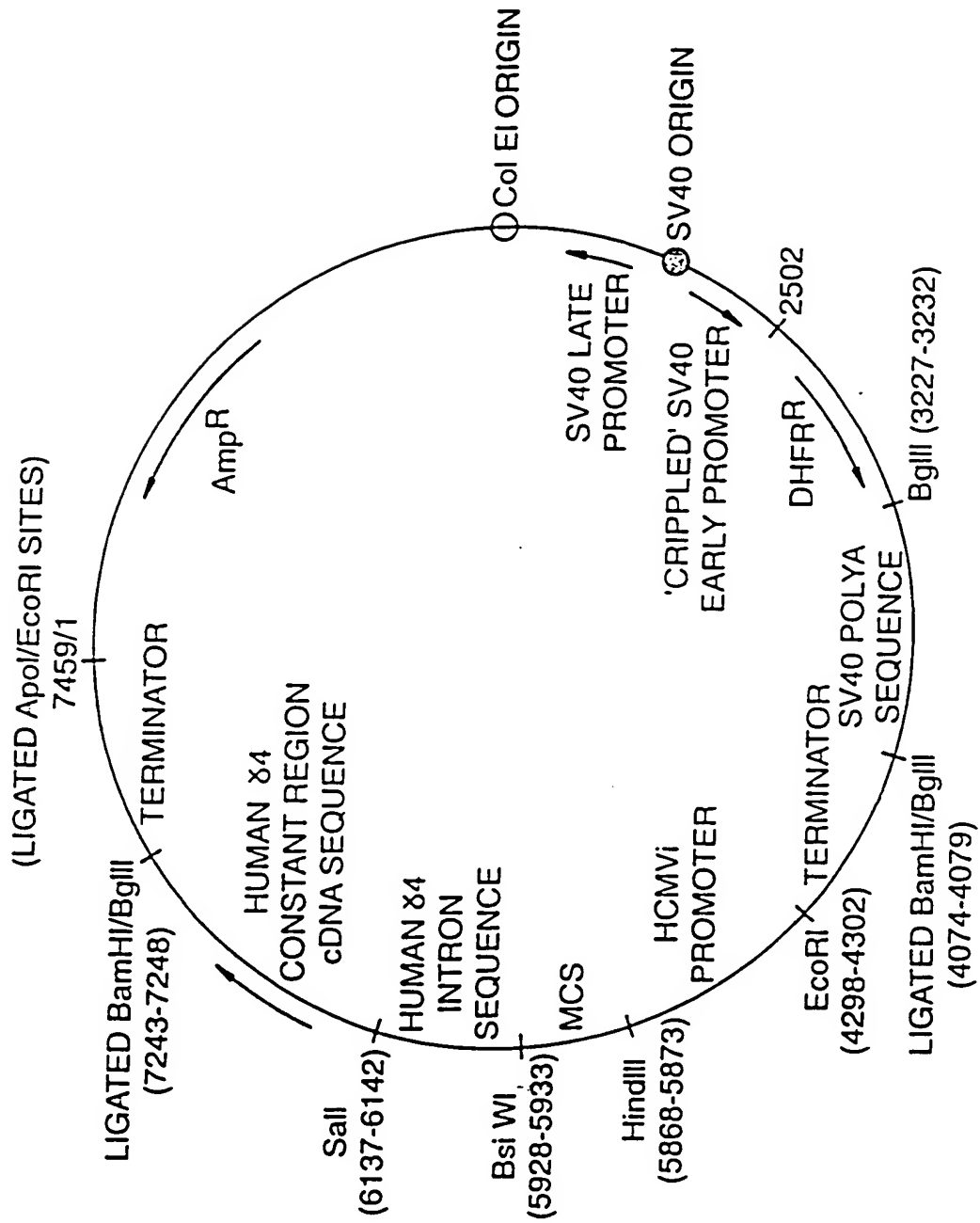
a K L A A T H D W T W R V F C L L A V A P -
  (SEQ ID NO:51)---
                                     B
                                     s
S                                     c
f                                     e
i                                     i
I                                     I
ggggcccaagccaggctgcaactgcagcagtcctggctgccaagggaaccacggtcacccgtct
61 -----+-----+-----+-----+-----+ 120
ccccgggtgtcggtccacgttgacgtcgctcagggccacgggttccccgggtgcacgtggcaga

a G A H S Q V Q L Q Q S G A K G P R S P S -
                                     B      E
                                     a      c
                                     n      o
                                     H      R
                                     I      I
cctcaggctgagtggatccgaatc
121 -----+-----+-----+-----+ 144
ggagtccactcacctaggttaag
      (SEQ ID NO:52)
a P Q V S G S E F -

```

FIGURE 5

Fig.6.



(SEQ ID NOS: 53-57)

H
 i
 n
 d
 I
 I
 I (SEQ ID NO:53) ---
 aaagcttcgccaccatgggatggagctgtatcaccctcttcttggtagcaacagctacagg
 1 -----+-----+-----+-----+-----+-----+ 60
 ttccgaagcggtaggtaccctaccctcgacatagtaggagaagaaccatcgttgcgatgtcc

 (SEQ ID NO:54) M G W S C I I L F L V A T A T
 taaggggtcacagttagcaggcttgaggctctggacatataatgggtgacaatgacatcc
 61 -----+-----+-----+-----+-----+ 120
 attccccgagtgtcatcgtccgaactccagaccggtatataaccactgttactgtagg

 A S
 P a
 a a
 L c
 I I
 actttgcctttctctccacagggtgtgcactccgacattgagctcaccacagtctccagaca
 121 -----+-----+-----+-----+-----+ 180
 tgaaacggaaagagagggtgtccacacgtgaggctgttaactcgagtgggtcagaggctctgt

 (SEQ ID NO:55) G V H S D I E L

 X B
 h a
 o m
 I H
 I I
 aaagctcgagctgaaacgtgagttagaattttaaacctttgcttccctcaattggatcc
 181 -----+-----+-----+-----+-----+ 234
 ttcgagctcgactttgcactcatctttaaatttgaaacgaaggagttaacctagg

 (SEQ ID NO:56) L E L K
 --- (SEQ ID NO:57)

FIGURE 7

Fig.8.

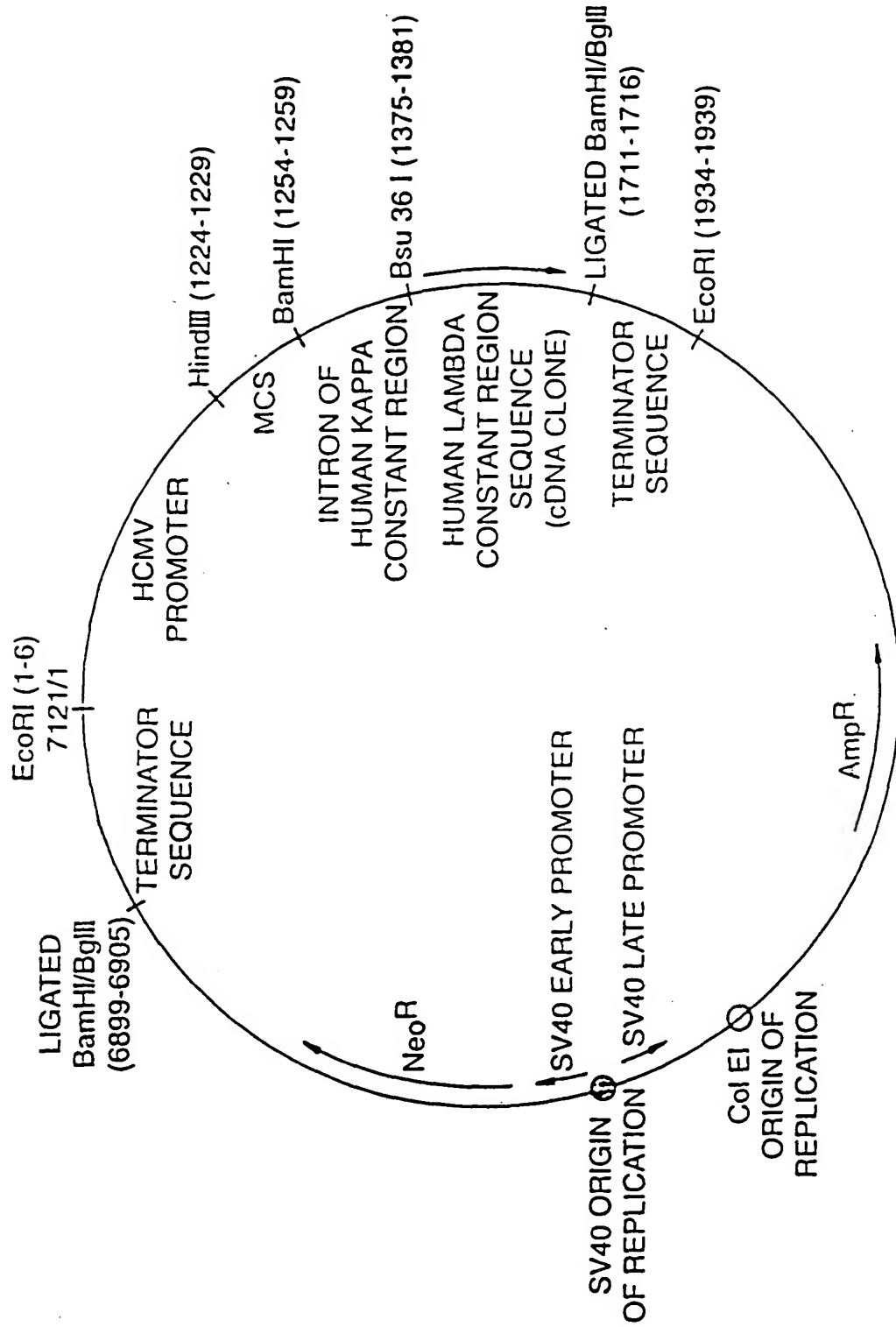


Fig.9.

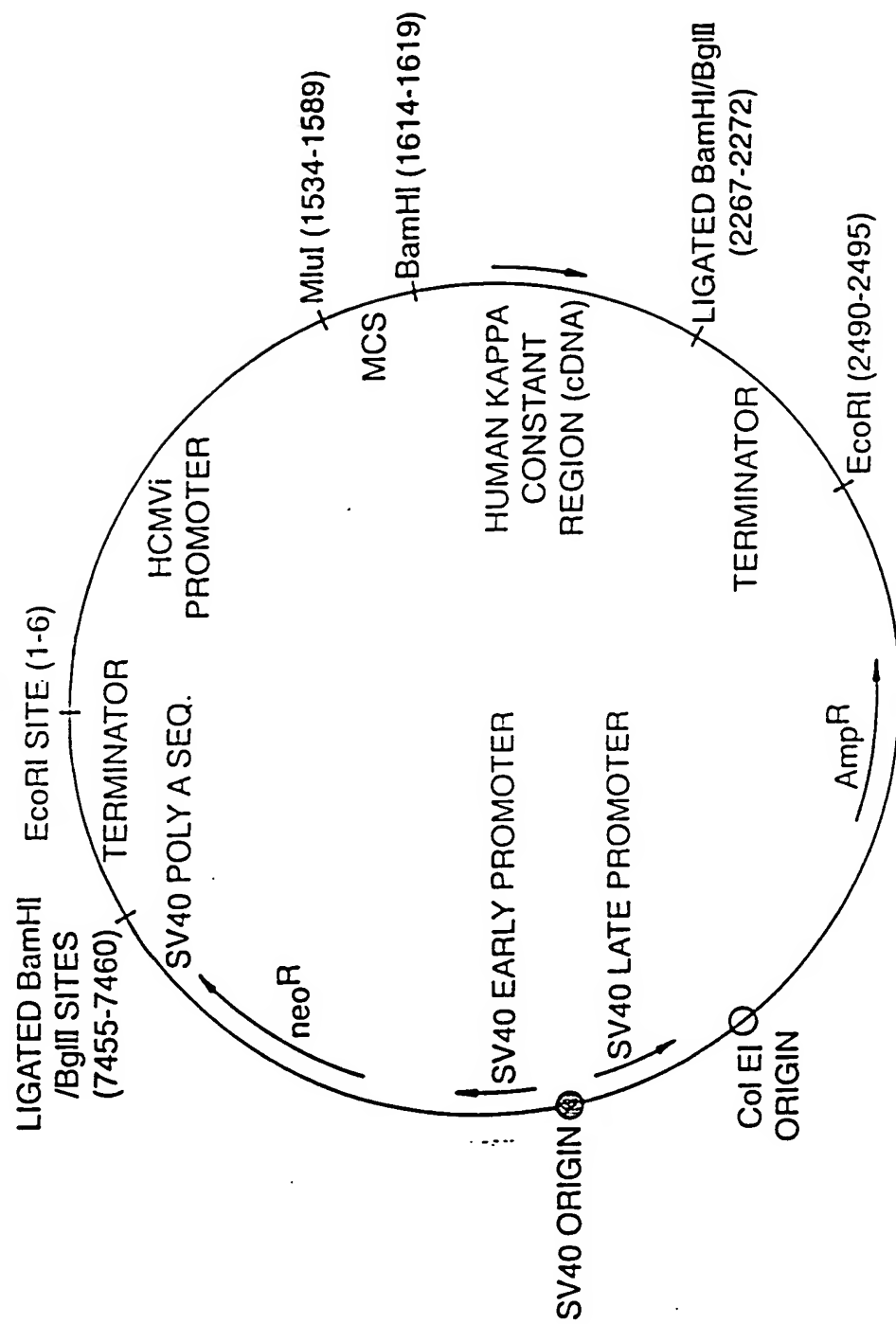


Fig.10.

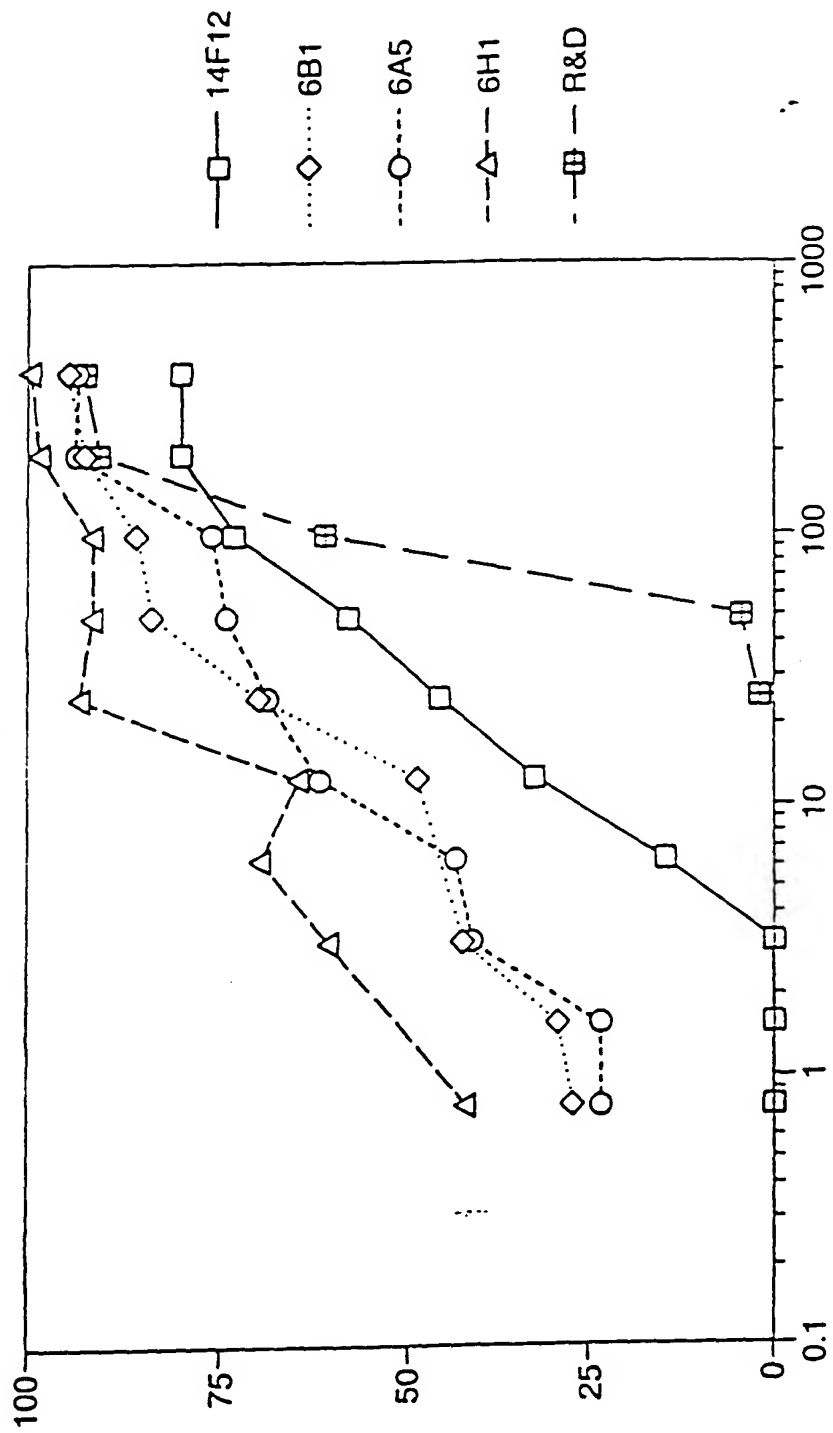


Fig.11.

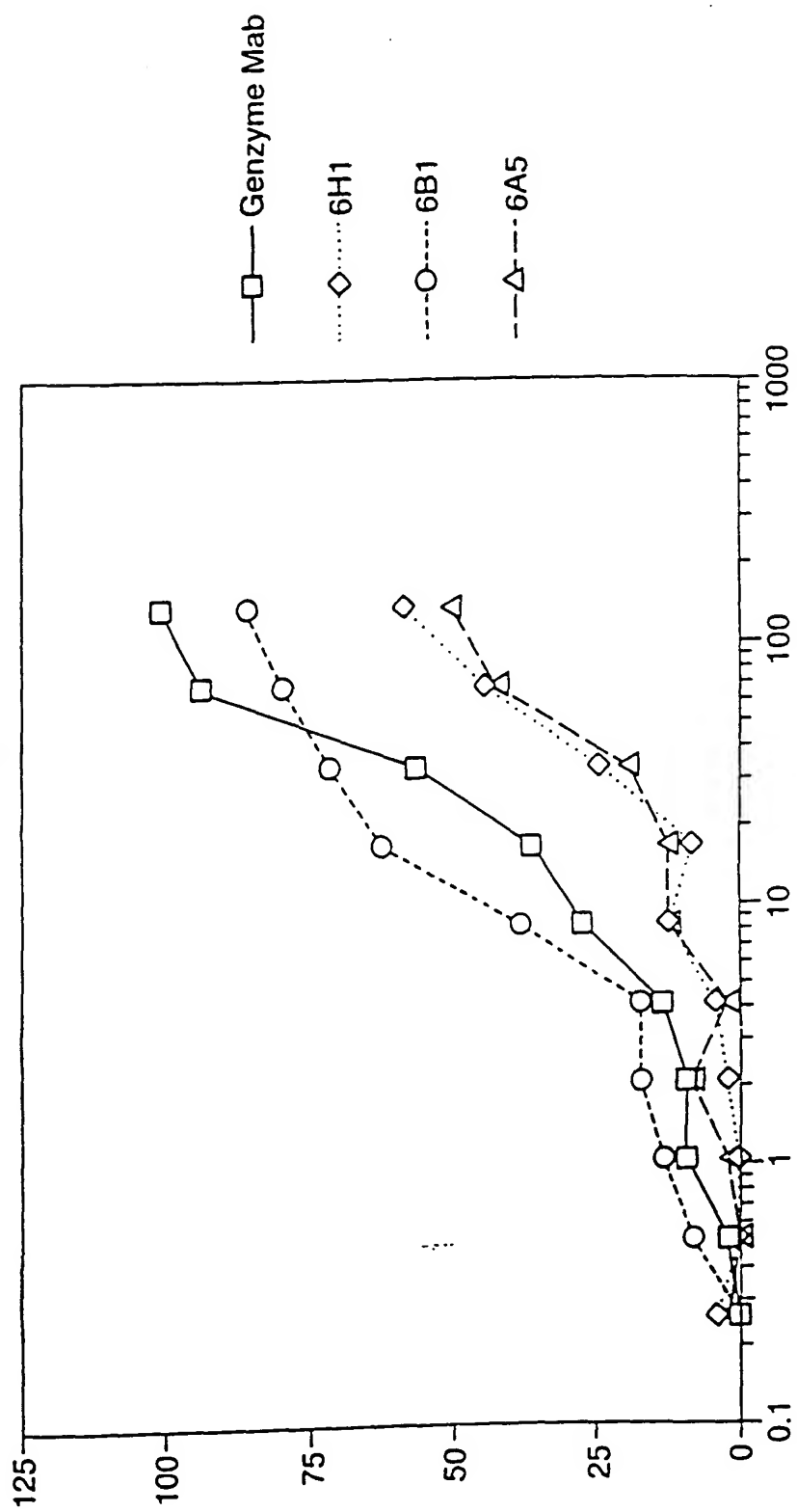


Fig.12.

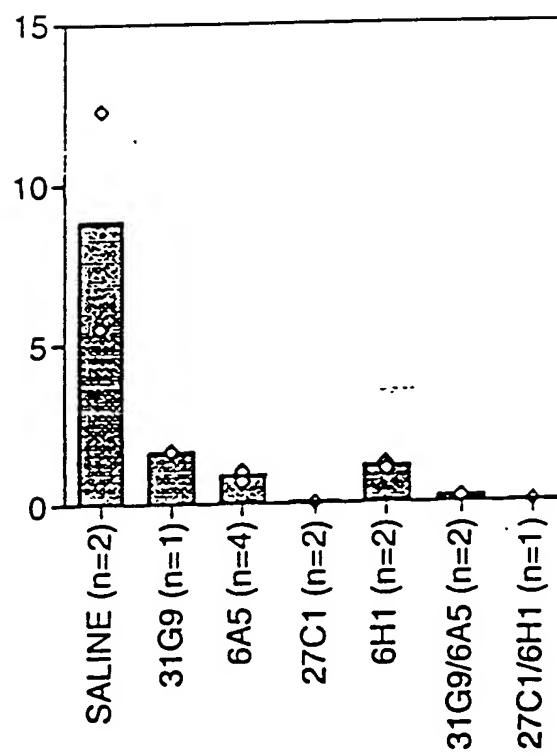
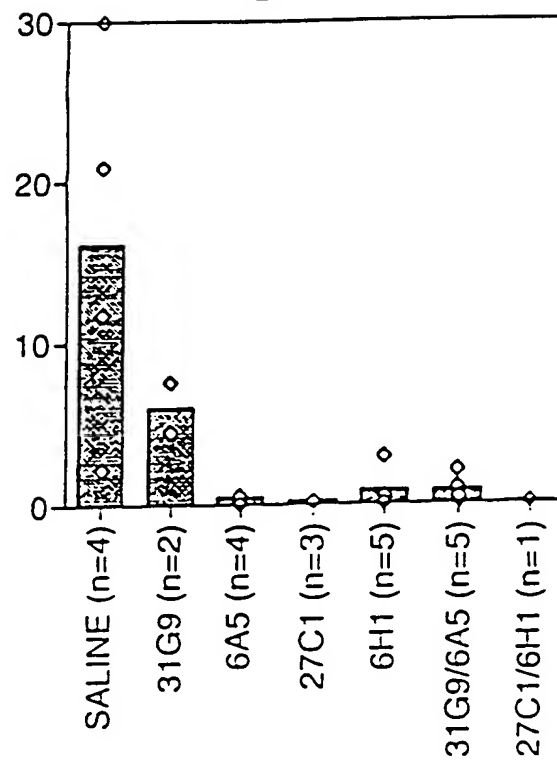


Fig.13(a).

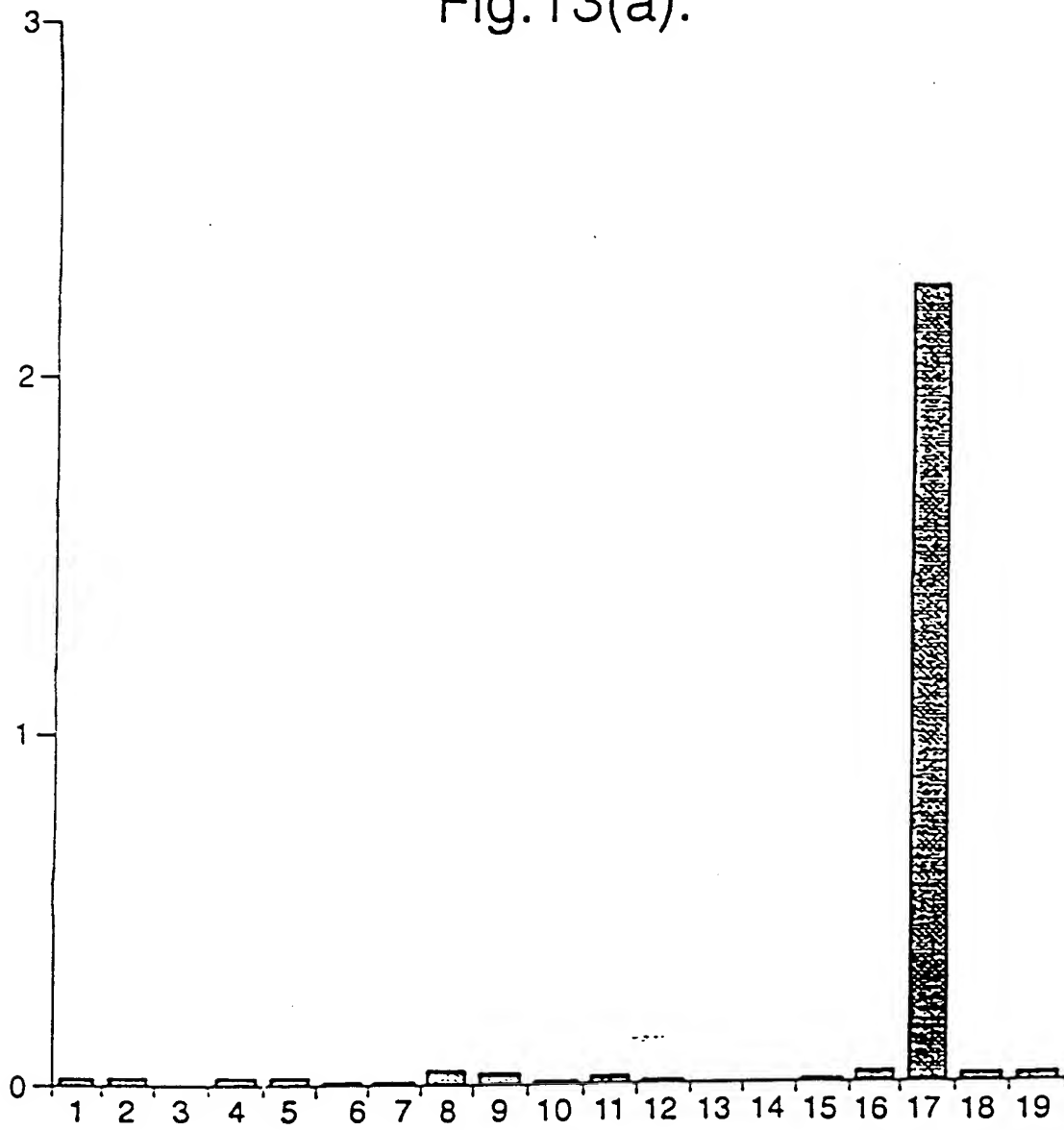


Fig.13(b).

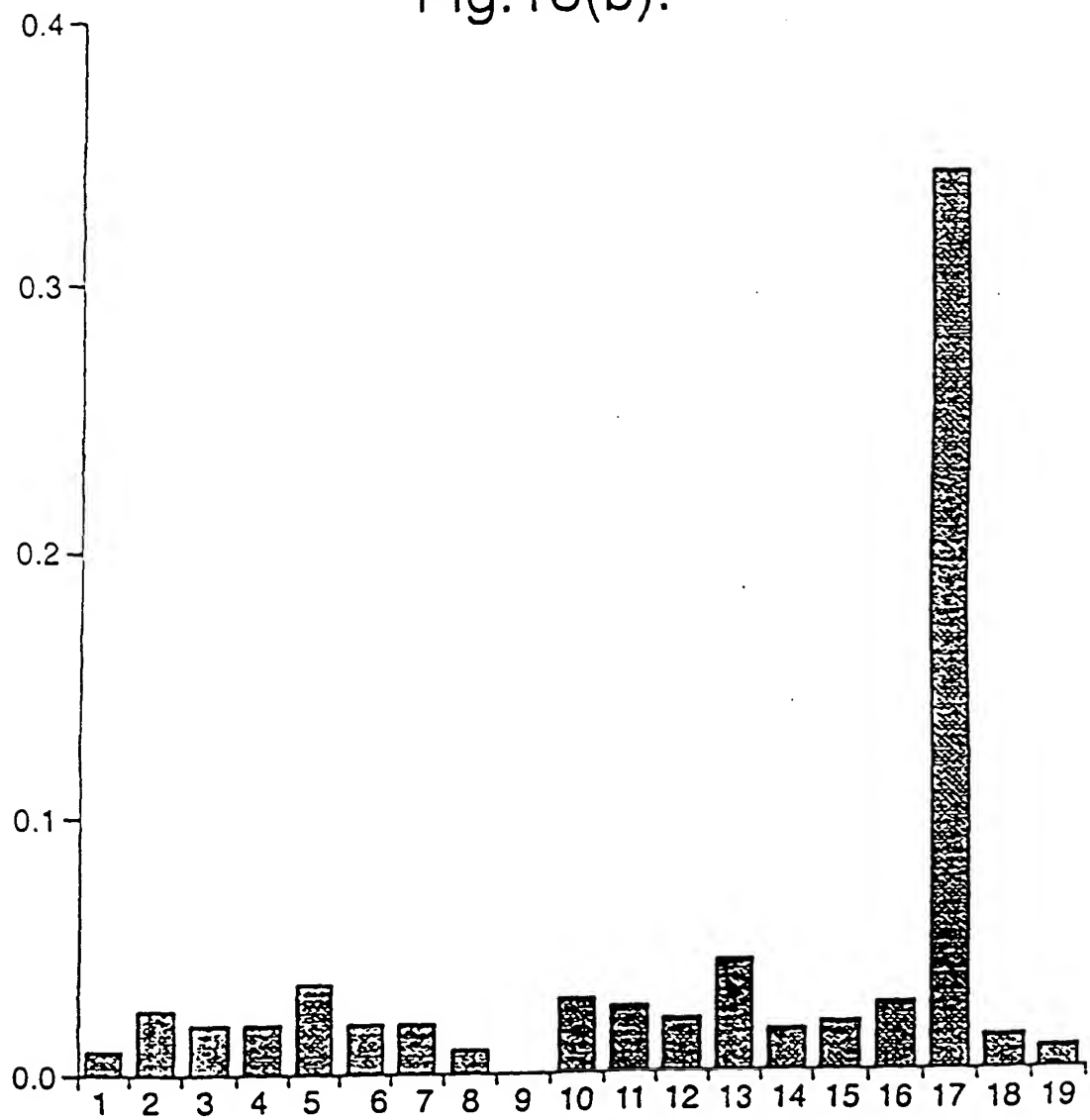


Figure 14

```

      10      20      30      40
GAA ATT GTG CTG ACT CAG TCT CCA TCC TCC TCT TCT GCA TCT GTA GGA
E I V L T Q S P S S L S A S V G>

      50      60      70      80      90
GAC AGA GTC ACC ATC ACT TGC CGG GCA AGT CAG GGC ATT GGA GAT GAT
D R V T I T C R A S Q G I G D D>

      100     110     120     130     140
TTG GGC TGG TAT CAG CAG AAG CCA GGG AAA GCC CCT ATC CTC CTG ATC
L G W Y Q Q Q K P G K A P I L L I>

      150     160     170     180     190
TAT GGT ACA TCC ACT TTA CAA AGT GGG GTC CCG TCA AGG TTC AGC GGC
Y G T S T L Q S G V P S R F S G>

      200     210     220     230     240
AGT GGA TCT GGC ACA GAT TTC ACT CTC ACC ATC AAC AGC CTG CAG CCT
S G S G T D F T L T I N S L Q P>

      250     260     270     280
GAA GAT TTT GCA ACT TAT TAC TGT CTA CAA GAT TCC AAT TAC CCG CTC
E D F A T Y Y C L Q D S N Y P L>

      290     300     310     320
ACT TTC GGC GGA GGG ACA CGA CTG GAG ATT AAA CGT (SEQ ID NO:58)
T F G G G T R L E I K R> (SEQ ID NO:59)

```


Fig.15.

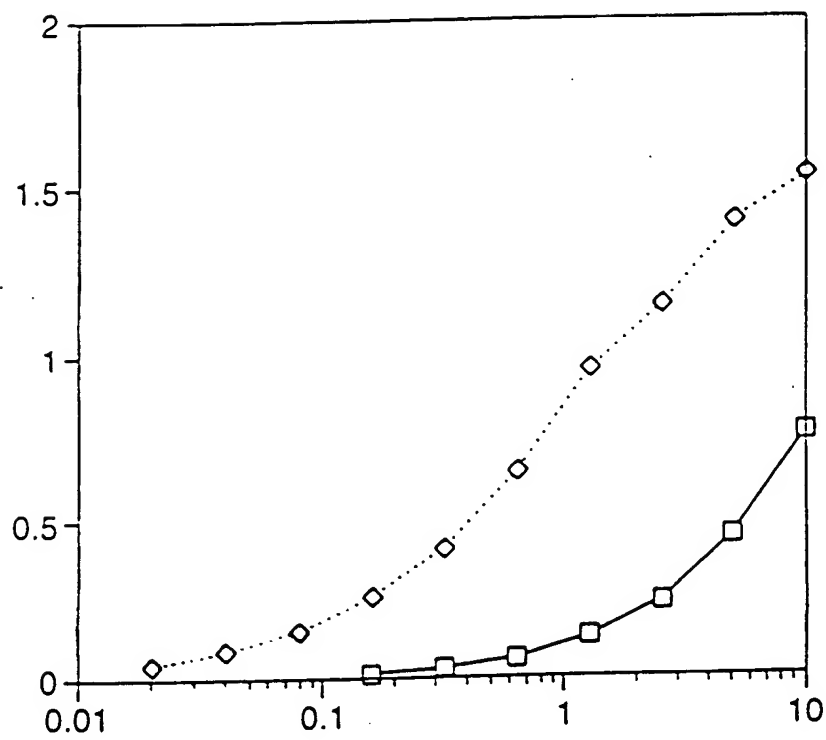


Fig.16.

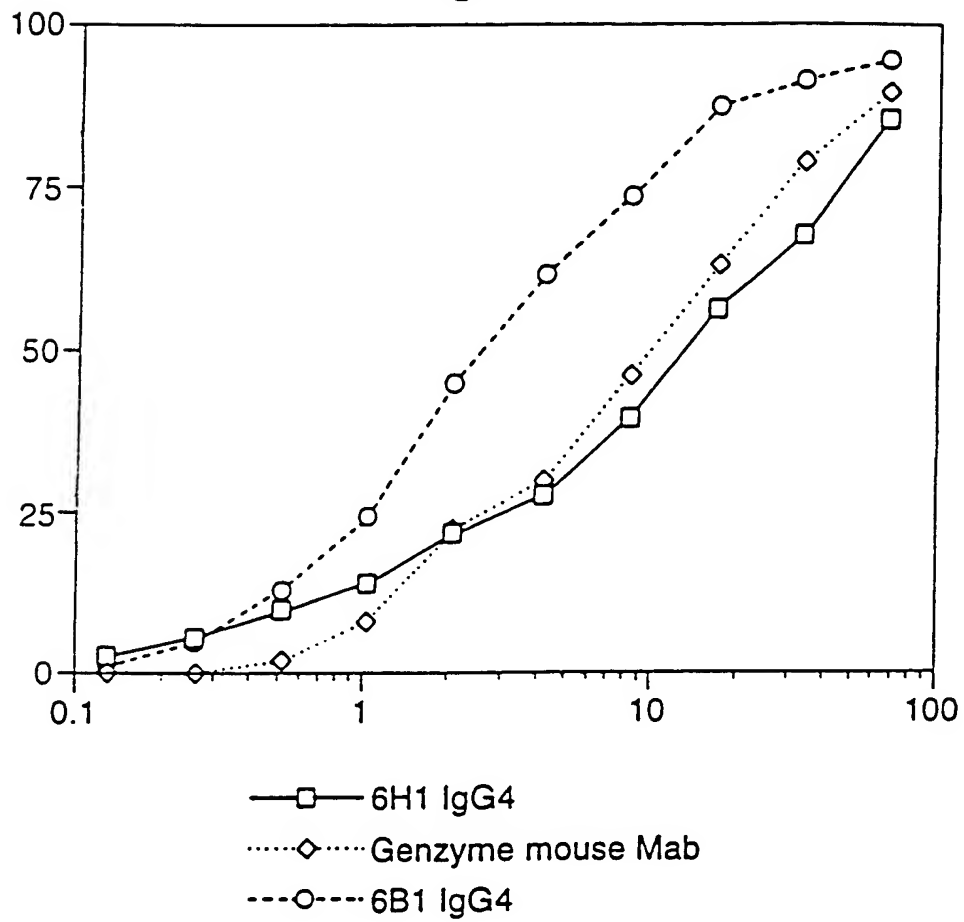


Fig.17.

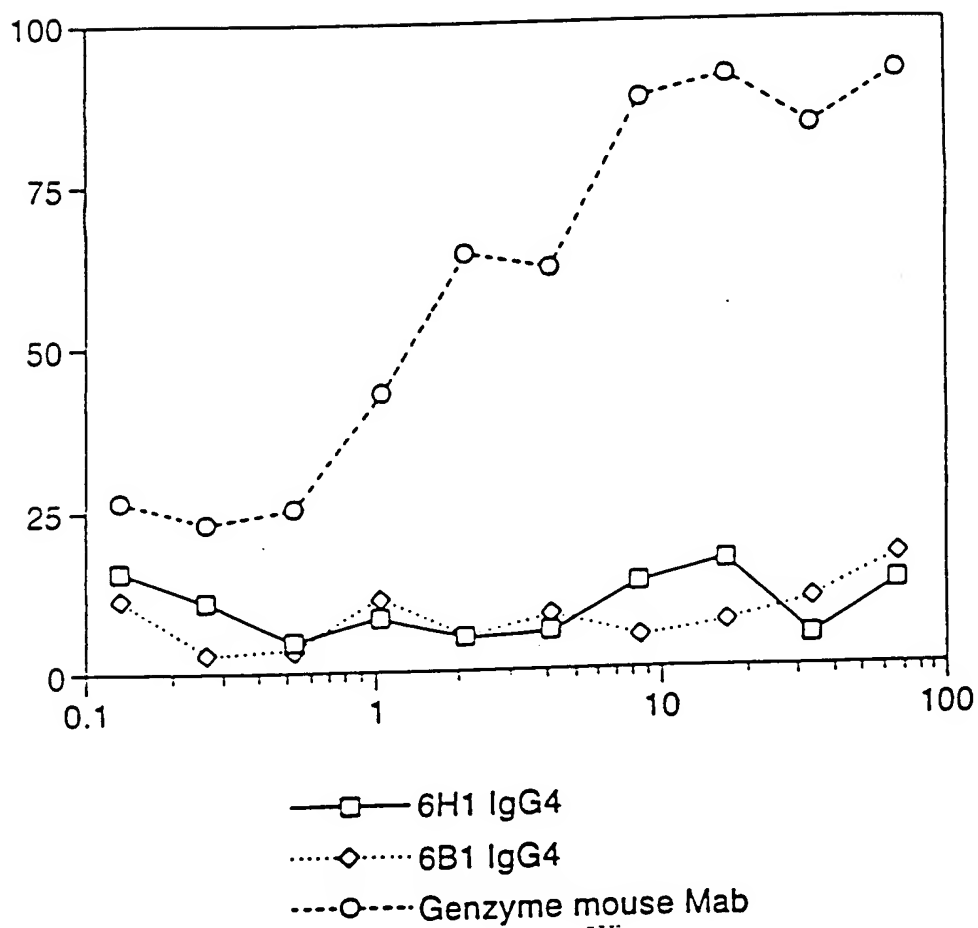


Fig.18.

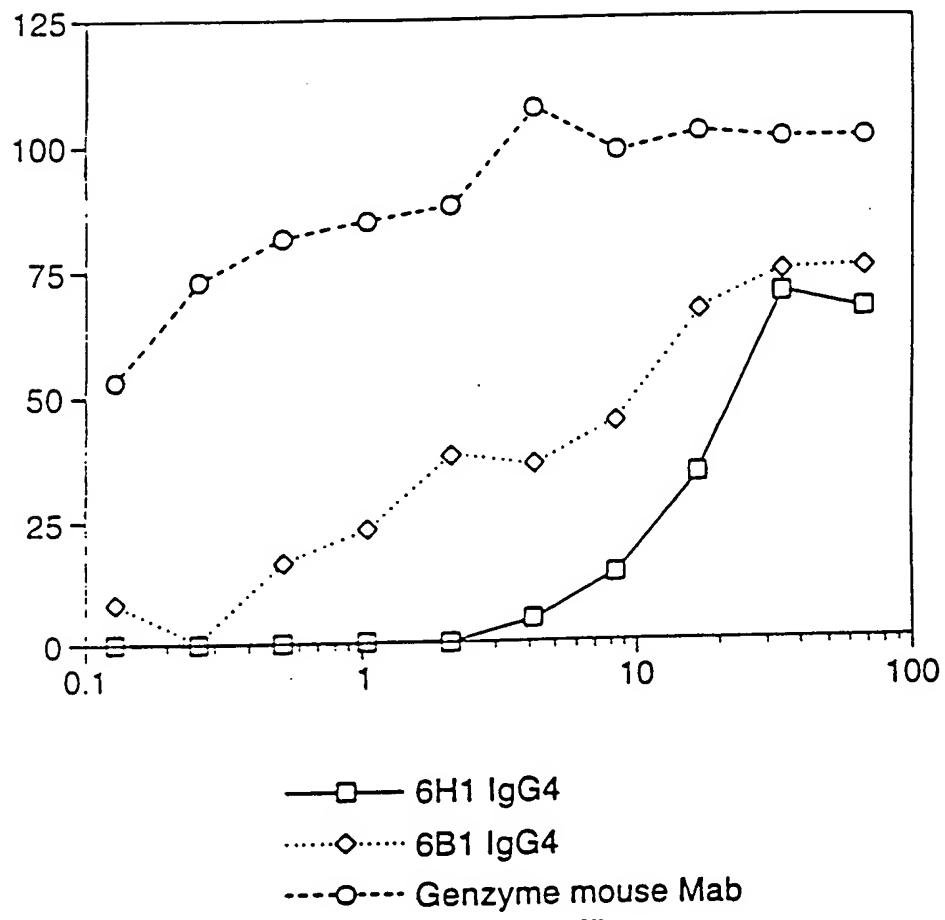


Figure 12

```

10      20      30      40
GAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTG GTC CAG CCT GGG AGG
E V Q L V E S G G G V V Q P G R>

50      60      70      80      90
TCC CTG AGA CTC TCC TGT GCA GCG TCT GGA TTC ACC TTC AGT AGC TAT
S L R L S C A A S G F T F S S Y>

100     110     120     130     140
GGC ATG CAC TGG GTC CGC CAG GCT CCA GGC GAG GGG CTG GAG TGG GTG
G M H W V R Q A P G K G L E W V>

150     160     170     180     190
GCA GTT ATA TGG TAT GAT GGA AGT AAT AAA TAC TAT GCA GAC TCC GTG
A V I W Y D G S N K Y Y A D S V>

200     210     220     230     240
AAG GGC CGA TTC ACC ATC TCC AGA GAC AAT TCC AAG AAC ACG CTG TAT
K G R F T I S R D N S K H T I Y>

250     260     270     280
CTG CAA ATG GAC AGC CTG AGA GCC GAG GAC ACG GCC GTG TAT TAC TGT
L Q M D S L R A E D T A V Y Y C>

290     300     310     320     330
GGA AGA ACG CTG GAG TCT AGT TTG TGG GGC CAA GGC ACC CTG GTC ACC
G R T L E S S L W G Q G T L V T>

340
GTC TCC TCA (SEQ ID NO:60)
V S S (SEQ ID NO:61)

```

Figure 19 (ii)

```

10      TCG TCT GAG CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG
      S  S  E  L  T  Q  D  P  A  V  S  V  A  L  G  Q>
20
30
40
50      ACA GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA
      T  V  R  I  T  C  Q  G  D  S  L  R  S  Y  Y  A>
60
70
80
90
100     AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC ATC TAT
      S  W  Y  Q  Q  K  P  G  Q  A  P  V  L  V  I  Y>
110
120
130
140
150     GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC CGA TTC TCT GGC TCC
      G  K  N  N  R  P  S  G  I  P  D  R  F  S  G  S>
160
170
180
190
200     AGC TCA GGA AAC ACA GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAA
      S  S  G  N  T  A  S  L  T  I  T  G  A  Q  A  E>
210
220
230
240
250     GAT GAG GCT GAC TAT TAC TGT AAC TCC CGG GAC AGC AGT AGT ACC CAT
      D  E  A  D  Y  Y  C  N  S  R  D  S  S  S  T  H>
260
270
280
290     CGA GGG GTG TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT (SEQ ID NO:62)
      R  G  V  F  G  G  G  T  K  L  T  V  L  G  G
300
310
320
330     (SEQ ID NO:63)

```

Figure 19 (iii)

```

10      TCG TCT GAG CTG ACT CAG GAC CCT GCT GTG TCT GTG GCC TTG GGA CAG
      S  S  E  L  T  Q  D  P  A  V  S  V  A  L  G  Q>
20
30
40
50      ACA GTC AGG ATC ACA TGC CAA GGA GAC AGC CTC AGA AGC TAT TAT GCA
      T  V  R  I  T  C  Q  G  D  S  L  R  S  Y  Y  A>
60
70
80
90
100     AGC TGG TAC CAG CAG AAG CCA GGA CAG GCC CCT GTA CTT GTC ATC TAT
      S  W  Y  Q  Q  Q  K  P  G  Q  A  P  V  L  V  I  Y>
110
120
130
140
150     GGT AAA AAC AAC CGG CCC TCA GGG ATC CCA GAC CGA TTC GCT GGC TCC
      G  K  N  N  R  P  S  G  I  P  D  R  F  A  G  S>
160
170
180
190
200     AAC TCA GGA AAC ACA GCT TCC TTG ACC ATC ACT GGG GCT CAG GCG GAG
      N  S  G  N  T  A  S  L  T  I  T  A  Q  A  E>
210
220
230
240
250     GAT GAG GCT GAC TAT TAC TGT AGC TCC CGG GAC AGC AGT GGT AAC CAT
      D  E  A  D  Y  Y  C  S  S  R  D  S  S  G  N  ID>
260
270
280
290     GTG GTT TTC GGC GGA GGG ACC AAG CTG ACC GTC CTA GGT (SEQ ID NO:64)
      V  V  F  G  G  G  T  K  L  T  V  L  G  (SEQ ID NO:65)
300
310
320

```

Figure 19(iv)

```

10      20      30      40
GAT GTT GTG ATG ACT CAG TCT CCA TCC TCT GCA TCT GTA GGA
D V V M T Q S P S L S A S V G>

50      60      70      80      90
GAC AGA GTC ACC ATC ACT TGC CGG GCC AGT CAG GGC ATT AGC AAT TAT
D R V T I T C R A S Q G I S N Y>

100     110     120     130     140
TTA GCC TGG TAT CAG CAA AAA CCA GGG AAA GCC CCT AAG CTC CTG ATC
L A W Y Q Q K P G K A P K L L I>

150     160     170     180     190
TAT AAG GCA TCT ACT TTA GAA AGT GGG GTC CCA TCA AGG TTC AGT GGC
Y K A S T L E S G V P S R F S G>

200     210     220     230     240
AGT GGA TCT GGG ACA GAA TTC ACT CTC ACA ATC AGC AGT CTG CAA CCT
S G S G T E F T L T I S S L Q P>

250     260     270     280
GAA GAT TTT GCA ACT TAC TAC TGT CAA CAG AGT TAC AGT ACC CCT CGA
E D F A T Y Y C Q Q S Y S T P R>

290     300     310     320
ACG TTC GGC CAA GGG ACC AAA GTG GAT ATC AAA CGT (SEQ ID NO:66)
T F G Q G T K V D I K R (SEQ ID NO:67)

```


Fig.20.

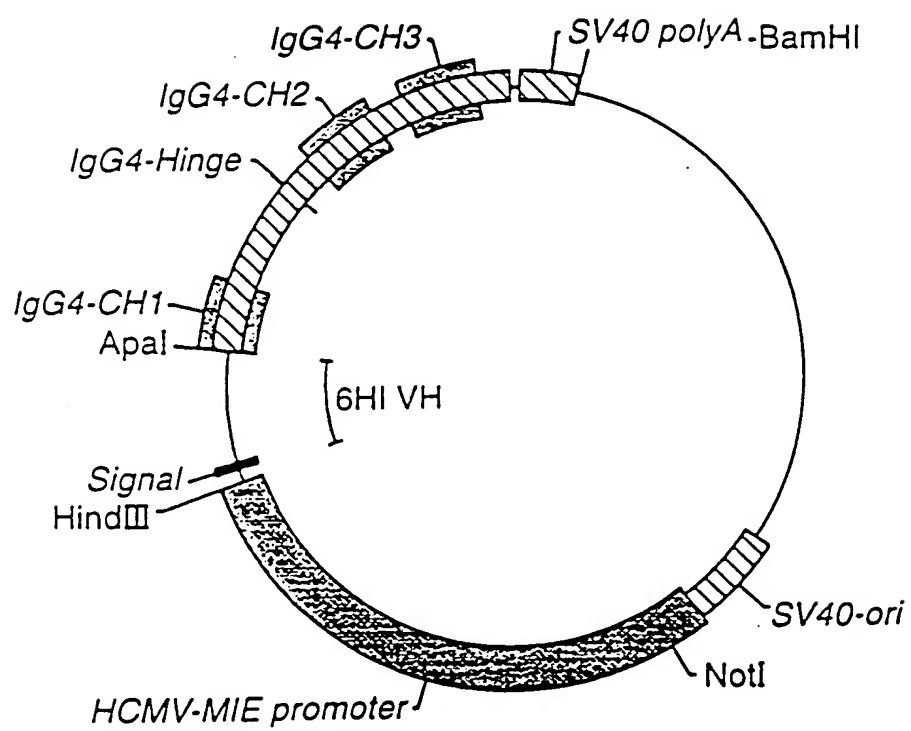


Fig.21.

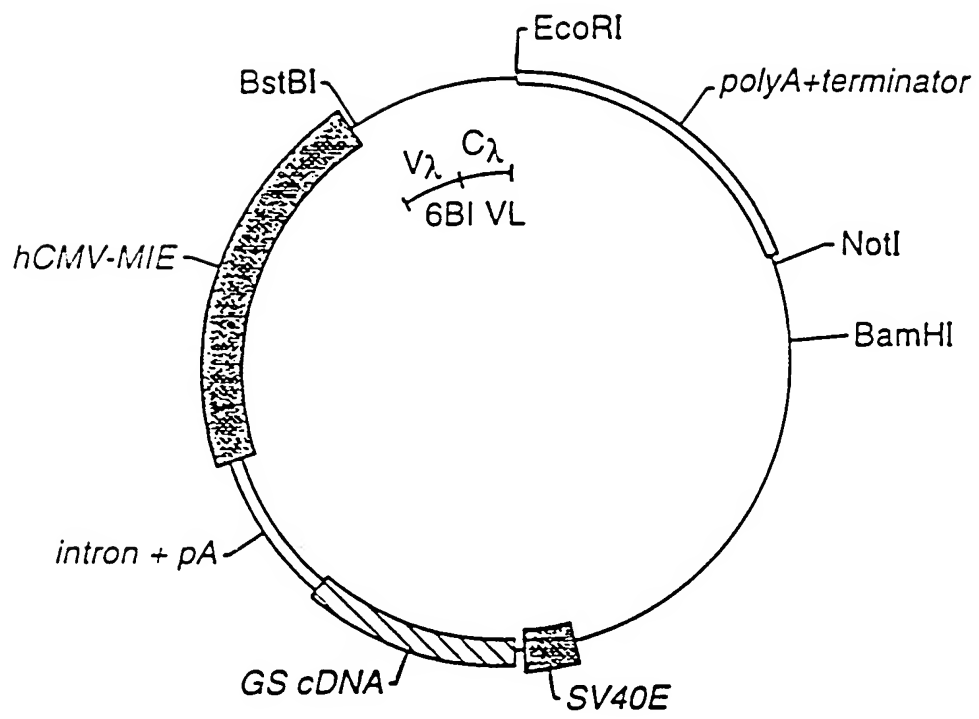


Fig.22.

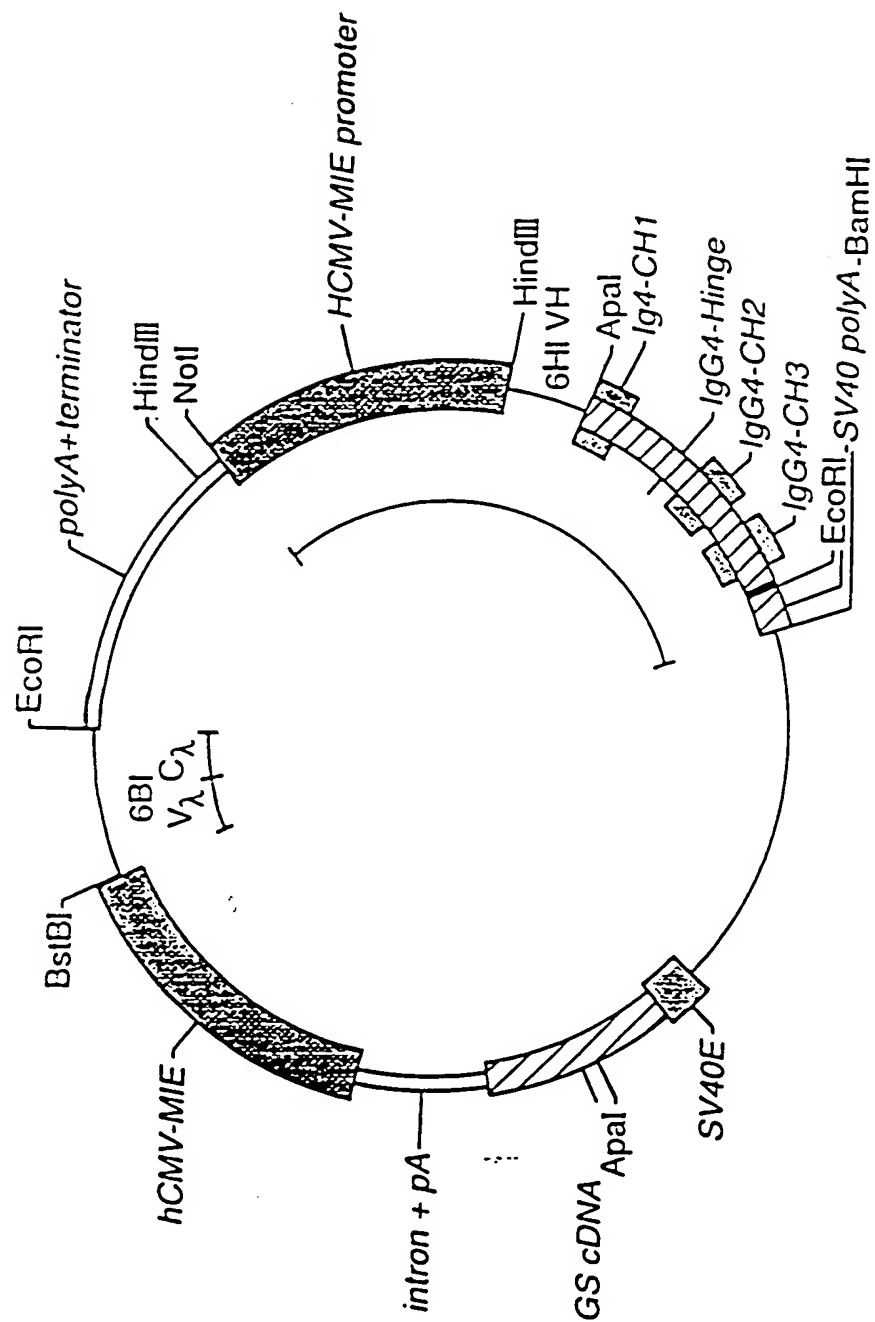
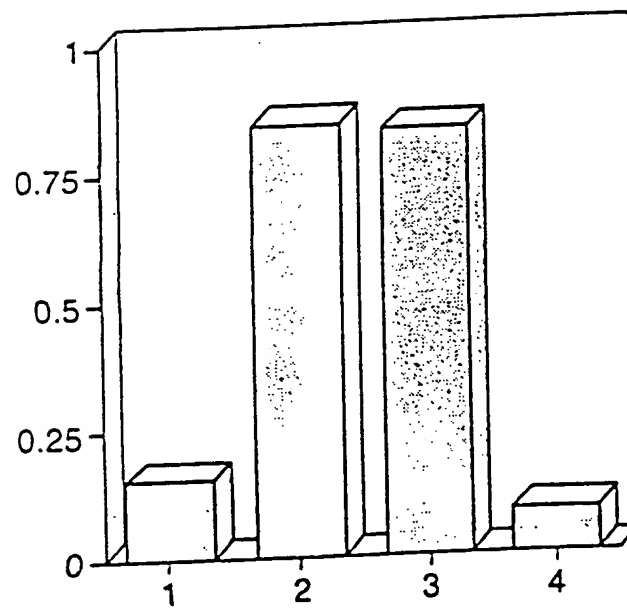


Fig.23.



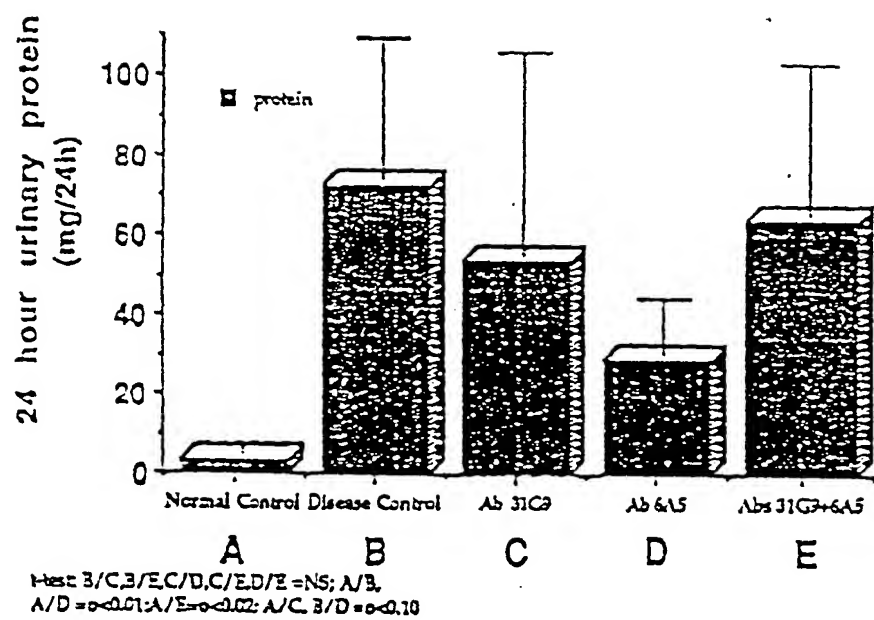


FIGURE 24

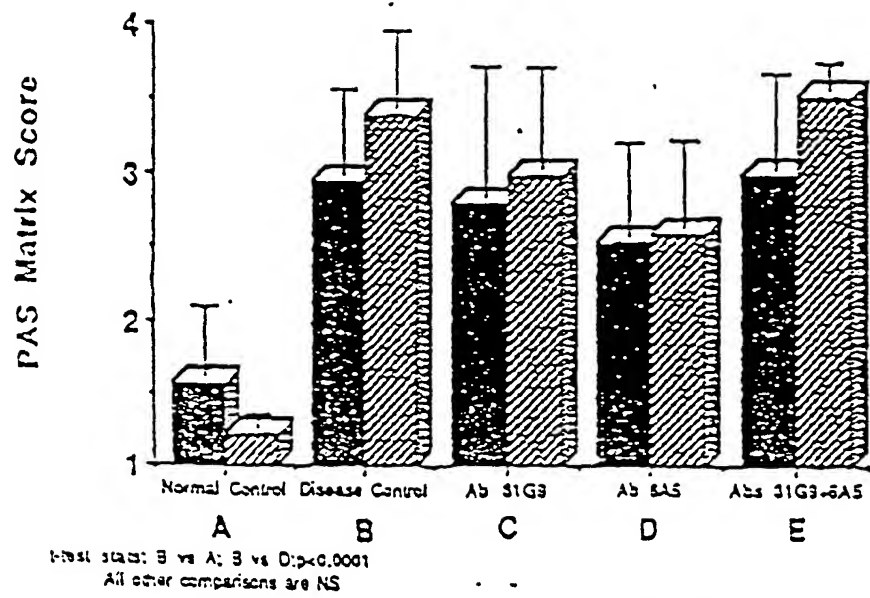


FIGURE 25